OIPE

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RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: US/09/900,590   TIME: 11:25:41

Input Set : N:\Crf3\RULE60\09900590.txt
Output Set: N:\CRF3\07202001\I900590.raw

SEQUENCE LISTING

ENTERED

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 4 (1) GENERAL INFORMATION:
 6       (i) APPLICANT: Huse, William D.
 7                     Glaser, Scott M.
 9      (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
10                              Antibodies, Nucleic Acids Encoding Same and Methods of
Use
12     (iii) NUMBER OF SEQUENCES: 100
14      (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Campbell & Flores LLP
16          (B) STREET: 4370 La Jolla Village Drive, Suite 700
17          (C) CITY: San Diego
18          (D) STATE: California
19          (E) COUNTRY: United States
20          (F) ZIP: 92122
22       (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28      (vi) CURRENT APPLICATION DATA:
C--> 29          (A) APPLICATION NUMBER: US/09/900,590
C--> 30          (B) FILING DATE: 06-Jul-2001
31          (C) CLASSIFICATION:
33     (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 09/016,061
35          (B) FILING DATE:
37    (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Campbell, Cathryn A.
39          (B) REGISTRATION NUMBER: 31,815
40          (C) REFERENCE/DOCKET NUMBER: P-IX 2965
42      (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: (619) 535-9001
44          (B) TELEFAX: (619) 535-8949
47 (2) INFORMATION FOR SEQ ID NO: 1:
49       (i) SEQUENCE CHARACTERISTICS:
50          (A) LENGTH: 351 base pairs
51          (B) TYPE: nucleic acid
52          (C) STRANDEDNESS: both
53          (D) TOPOLOGY: linear
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 1..351
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG        48
64 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
65  1               5                   10                  15
67 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT        96
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 68 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 69             20                  25                  30
 71 GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC      144
 72 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 73             35                  40                  45
 75 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
 76 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
 77         50                  55                  60
 79 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC      240
 80 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 81 65                  70                  75                  80
 83 CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT      288
 84 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85                 85                  90                  95
 87 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA      336
 88 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
 89             100                 105                 110
 91 GTG ACT GTT TCT AGT                                                  351
 92 Val Thr Val Ser Ser
 93         115
 96 (2) INFORMATION FOR SEQ ID NO: 2:
 98      (i) SEQUENCE CHARACTERISTICS:
 99          (A) LENGTH: 117 amino acids
100          (B) TYPE: amino acid
101          (D) TOPOLOGY: linear
103     (ii) MOLECULE TYPE: protein
105     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
107 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
108  1               5                  10                  15
110 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
111             20                  25                  30
113 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
114             35                  40                  45
116 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
117         50                  55                  60
119 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
120 65                  70                  75                  80
122 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
123                 85                  90                  95
125 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
126             100                 105                 110
128 Val Thr Val Ser Ser
129         115
131 (2) INFORMATION FOR SEQ ID NO: 3:
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 321 base pairs
135          (B) TYPE: nucleic acid
136          (C) STRANDEDNESS: both
137          (D) TOPOLOGY: linear
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PATENT APPLICATION: US/09/900,590   TIME: 11:25:41

Input Set : N:\Crf3\RULE60\09900590.txt
Output Set: N:\CRF3\07202001\I900590.raw

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140      (ix) FEATURE:
141           (A) NAME/KEY: CDS
142           (B) LOCATION: 1..321
145      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
147 GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA         48
148 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
149  1               5                  10                  15
151 GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC         96
152 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
153          20                  25                  30
155 CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC        144
156 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
157          35                  40                  45
159 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC        192
160 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
161          50                  55                  60
163 AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT        240
164 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
165  65                  70                  75                  80
167 GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC        288
168 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
169          85                  90                  95
171 ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG                            321
172 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
173          100                 105
176 (2) INFORMATION FOR SEQ ID NO: 4:
178      (i) SEQUENCE CHARACTERISTICS:
179           (A) LENGTH: 107 amino acids
180           (B) TYPE: amino acid
181           (D) TOPOLOGY: linear
183      (ii) MOLECULE TYPE: protein
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
187 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
188  1               5                  10                  15
190 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
191          20                  25                  30
193 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
194          35                  40                  45
196 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
197          50                  55                  60
199 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
200  65                  70                  75                  80
202 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
203          85                  90                  95
205 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
206          100                 105
208 (2) INFORMATION FOR SEQ ID NO: 5:
210      (i) SEQUENCE CHARACTERISTICS:
211           (A) LENGTH: 351 base pairs
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212            (B) TYPE: nucleic acid
213            (C) STRANDEDNESS: both
214            (D) TOPOLOGY: linear
217       (ix) FEATURE:
218            (A) NAME/KEY: CDS
219            (B) LOCATION: 1..351
222       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
224 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG        48
225 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
226  1               5                  10                  15
228 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT        96
229 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
230             20                  25                  30
232 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC       144
233 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
234         35                  40                  45
236 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG       192
237 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
238     50                  55                  60
240 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC       240
241 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
242  65                  70                  75                  80
244 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT       288
245 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
246             85                  90                  95
248 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG       336
249 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
250            100                 105                 110
252 GTC ACT GTC TCT GCA                                                   351
253 Val Thr Val Ser Ala
254         115
257 (2) INFORMATION FOR SEQ ID NO: 6:
259      (i) SEQUENCE CHARACTERISTICS:
260            (A) LENGTH: 117 amino acids
261            (B) TYPE: amino acid
262            (D) TOPOLOGY: linear
264      (ii) MOLECULE TYPE: protein
266      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
268 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
269  1               5                  10                  15
271 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
272             20                  25                  30
274 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
275         35                  40                  45
277 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
278     50                  55                  60
280 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
281  65                  70                  75                  80
283 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
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284                     85                  90                  95
286 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
287          100                 105                 110
289 Val Thr Val Ser Ala
290          115
292 (2) INFORMATION FOR SEQ ID NO: 7:
294      (i) SEQUENCE CHARACTERISTICS:
295           (A) LENGTH: 321 base pairs
296           (B) TYPE: nucleic acid
297           (C) STRANDEDNESS: both
298           (D) TOPOLOGY: linear
301      (ix) FEATURE:
302           (A) NAME/KEY: CDS
303           (B) LOCATION: 1..321
306      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
308 GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT GTG ACA CCA GGA       48
309 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
310   1               5                  10                  15
312 GAT AGC GTC AGT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC       96
313 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
314          20                  25                  30
316 CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA AGG CTT CTC ATC      144
317 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
318          35                  40                  45
320 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC TCC AGG TTC AGT GGC      192
321 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
322          50                  55                  60
324 AGT GGA TCA GGG ACA GAT TTC GCT CTC AGT ATC AAC AGT GTG GAG ACT      240
325 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
326   65                  70                  75                  80
328 GAA GAT TTT GGA ATG TAT TTC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
329 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
330          85                  90                  95
332 ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG                          321
333 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
334          100                 105
337 (2) INFORMATION FOR SEQ ID NO: 8:
339      (i) SEQUENCE CHARACTERISTICS:
340           (A) LENGTH: 107 amino acids
341           (B) TYPE: amino acid
342           (D) TOPOLOGY: linear
344      (ii) MOLECULE TYPE: protein
346      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
348 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
349   1               5                  10                  15
351 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
352          20                  25                  30
354 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
355          35                  40                  45
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VERIFICATION SUMMARY   DATE: 07/20/2001
PATENT APPLICATION: US/09/900,590   TIME: 11:25:42

Input Set : **N:\Crf3\RULE60\09900590.txt**
Output Set: **N:\CRF3\07202001\I900590.raw**

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
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